0590
c905

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/938,330

DATE: 09/10/2001
TIME: 09:23:46

Input Set : A:\LEX-0221-USA SEQLIST.txt
Output Set: N:\CRF3\09102001\I938330.raw

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 4 <110> APPLICANT: Walke, D. Wade
 5        Hilbun, Erin
 6        Scoville, John
 7        Friddle, Carl Johan
 8        Hu, Yi
 9        Turner, C. Alexander Jr.
11 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
13 <130> FILE REFERENCE: LEX-0237-USA
15 <140> CURRENT APPLICATION NUMBER: US/09/938,330
15 <141> CURRENT FILING DATE: 2001-08-22
15 <150> PRIOR APPLICATION NUMBER: US 60/227,104
16 <151> PRIOR FILING DATE: 2000-08-22
18 <150> PRIOR APPLICATION NUMBER: US 60/233,796
19 <151> PRIOR FILING DATE: 2000-09-19
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1356
27 <212> TYPE: DNA
28 <213> ORGANISM: homo sapiens
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32 gccgcgggca gccggacccc agagctgcac ctctctggaa agctcagtga ctatggtgtg     120
33 acagtgccct gcagcacaga ctttcgggga cgcttcctct cccacgtggt gtctggccca     180
34 gcagcagcct ctgcagggag catggtagtg gacacgccac ccacactacc acgacactcc     240
35 agtcacctcc gggtggctcg cagccctctg cacccaggag ggaccctgtg gcctggcagg     300
36 gtggggcgcc actccctcta cttcaatgtc actgttttcg ggaaggaact gcacttgcgc     360
37 ctgcggccca atcggaggtt ggtagtgcca ggatcctcag tggagtggca ggaggatttt     420
38 cgggagctgt tccggcagcc cttacggcag gagtgtgtgt acactggagg tgtcactgga     480
39 atgcctgggg cagctgttgc catcagcaac tgtgacggat tggcgggcct catccgcaca     540
40 gacagcaccg acttcttcat tgagcctctg gagcggggcc agcaggagaa ggaggccagc     600
41 gggaggacac atgtggtgta ccgccgggag gccgtccagc aggagtgggc agaacctgac     660
42 ggggacctgc acaatgaagc ctttggcctg ggagaccttc ccaacctgct gggcctggtg     720
43 ggggaccagc tgggcgacac agagcggaag cggcggcatg ccaagccagg cagctacagc     780
44 atcgaggtgc tgctggtggt ggacgactcg gtggttcgct tccatggcaa ggagcatgtg     840
45 cagaactatg tcctcaccct catgaatatc gtagatgaga tttaccacga tgagtccctg     900
46 ggggttcata taaatattgc cctcgtccgc ttgatcatgg ttggctaccg acagtccctg     960
47 agcctgatcg agcgcgggaa cccctcacgc agcctggagc aggtgtgtcg ctgggcacac    1020
48 tcccagcagc gccaggaccc cagccacgct gagcaccatg accacgttgt gttcctcacc    1080
49 cggcaggact ttgggccctc agggtatgca cccgtcactg gcatgtgtca ccccctgagg    1140
50 agctgtgccc tcaaccatga ggatggcttc tcctcagcct tcgtgatagc tcatgagacc    1200
51 ggccacgtgc tcggcatgga gcatgacggt caggggaatg gctgtgcaga tgagaccagc    1260
52 ctgggcagcg tcatggcgcc cctggtgcag gctgccttcc accgcttcca ttggtcccgc    1320
53 tgcagcaagc tggagctcag ccgctacctc ccgtag                              1356
55 <210> SEQ ID NO: 2
56 <211> LENGTH: 451
57 <212> TYPE: PRT
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RAW SEQUENCE LISTING
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Input Set : A:\LEX-0221-USA SEQLIST.txt
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 63 Ala Leu Cys Ala Ala Ala Gly Ser Arg Thr Pro Glu Leu His Leu Ser
 64             20                  25                  30
 65 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
 66         35                  40                  45
 67 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
 68     50                  55                  60
 69 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
 70 65                  70                  75                  80
 71 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
 72                 85                  90                  95
 73 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
 74             100                 105                 110
 75 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
 76             115                 120                 125
 77 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
 78         130                 135                 140
 79 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
 80 145                 150                 155                 160
 81 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
 82             165                 170                 175
 83 Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
 84             180                 185                 190
 85 Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
 86         195                 200                 205
 87 Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
 88     210                 215                 220
 89 Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
 90 225                 230                 235                 240
 91 Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
 92             245                 250                 255
 93 Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
 94             260                 265                 270
 95 Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
 96         275                 280                 285
 97 Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
 98     290                 295                 300
 99 Asn Ile Ala Leu Val Arg Leu Ile Met Val Gly Tyr Arg Gln Ser Leu
100 305                 310                 315                 320
101 Ser Leu Ile Glu Arg Gly Asn Pro Ser Arg Ser Leu Glu Gln Val Cys
102             325                 330                 335
103 Arg Trp Ala His Ser Gln Gln Arg Gln Asp Pro Ser His Ala Glu His
104         340                 345                 350
105 His Asp His Val Val Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly
106         355                 360                 365
107 Tyr Ala Pro Val Thr Gly Met Cys His Pro Leu Arg Ser Cys Ala Leu
```

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108      370                    375                  380
109 Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Ile Ala His Glu Thr
110 385              390              395                  400
111 Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Gly Cys Ala
112               405              410                  415
113 Asp Glu Thr Ser Leu Gly Ser Val Met Ala Pro Leu Val Gln Ala Ala
114           420              425              430
115 Phe His Arg Phe His Trp Ser Arg Cys Ser Lys Leu Glu Leu Ser Arg
116      435              440                  445
117 Tyr Leu Pro
118      450
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 894
122 <212> TYPE: DNA
123 <213> ORGANISM: homo sapiens
125 <400> SEQUENCE: 3
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127 gccgcgggca gccggacccc agagctgcac ctctctggaa agctcagtga ctatggtgtg     120
128 acagtgccct gcagcacaga ctttcgggga cgcttcctct cccacgtggt gtctggccca     180
129 gcagcagcct ctgcagggag catggtagtg gacacgccac ccacactacc acgacactcc     240
130 agtcacctcc gggtggctcg cagccctctg cacccaggag ggaccctgtg gcctggcagg     300
131 gtggggcgcc actccctcta cttcaatgtc actgttttcg ggaaggaact gcacttgcgc     360
132 ctgcggccca atcggaggtt ggtagtgcca ggatcctcag tggagtggca ggaggatttt     420
133 cgggagctgt tccggcagcc cttacggcag gagtgtgtgt acactggagg tgtcactgga     480
134 atgcctgggg cagctgttgc catcagcaac tgtgacggat ggcggggcct catccgcaca     540
135 gacagcaccg acttcttcat tgagcctctg gagcgggggcc agcaggagaa ggaggccagc     600
136 gggaggacac atgtggtgta ccgccgggag gccgtccagc aggagtgggc agaacctgac     660
137 ggggacctgc acaatgaagc ctttggcctg ggagaccttc ccaacctgct gggcctggtg     720
138 ggggaccagc tggcgacac agagcggaag cggcggcatg ccaagccagg cagctacagc     780
139 atcgaggtgc tgctggtggt ggacgactcg gtggttcgct tccatggcaa ggagcatgtg     840
140 cagaactatg tcctcaccct catgaatatc gtgtgcttac agggaagtcc ataa          894
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 297
144 <212> TYPE: PRT
145 <213> ORGANISM: homo sapiens
147 <400> SEQUENCE: 4
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151               20              25                  30
152 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
153           35              40              45
154 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
155      50              55              60
156 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
157 65              70              75                  80
158 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
159           85              90                  95
160 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
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161                 100                 105                 110
162 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
163         115                 120                 125
164 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
165         130                 135                 140
166 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
167 145                 150                 155                 160
168 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
169                 165                 170                 175
170 Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
171                 180                 185                 190
172 Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
173         195                 200                 205
174 Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
175         210                 215                 220
176 Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
177 225                 230                 235                 240
178 Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
179                 245                 250                 255
180 Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
181         260                 265                 270
182 Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
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185         290                 295
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188 <211> LENGTH: 1461
189 <212> TYPE: DNA
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195 acagtgccct gcagcacaga ctttcgggga cgcttcctct cccacgtggt gtctggccca     180
196 gcagcagcct ctgcagggag catggtagtg gacacgccac ccacactacc acgacactcc     240
197 agtcacctcc gggtggctcg cagccctctg cacccaggag ggaccctgtg gcctggcagg     300
198 gtggggcgcc actccctcta cttcaatgtc actgttttcg ggaaggaact gcacttgcgc     360
199 ctgcggccca atcggaggtt ggtagtgcca ggatcctcag tggagtggca ggaggatttt     420
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207 cagaactatg tcctcaccct catgaatatc gtagatgaga tttaccacga tgagtccctg     900
208 ggggttcata taaatattgc cctcgtccgc ttgatcatgg ttggctaccg acagtccctg     960
209 agcctgatcg agcgcgggaa cccctcacgc agcctggagc aggtgtgtcg ctgggcacac    1020
210 tcccagcagc gccaggaccc cagccacgct gagcaccatg accacgttgt gttcctcacc    1080
211 cggcaggact ttgggccctc agggtatgca cccgtcactg gcatgtgtca cccctgagg    1140
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212  agctgtgccc tcaaccatga ggatggcttc tcctcagcct tcgtgatagc tcatgagacc   1200
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214  ctgggcagcg tcatggcgcc cctggtgcag gctgccttcc accgcttcca ttggtcccgc   1320
215  tgcagcaagc tggagctcag ccgctacctc ccctcctacg actgcctcct cgatgacccc   1380
216  tttgatcctg ccacctgccc gggcggccgc tcgagcccta tagtgagtcg tattaggatg   1440
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220 <211> LENGTH: 486
221 <212> TYPE: PRT
222 <213> ORGANISM: homo sapiens
224 <400> SEQUENCE: 6

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228               20                  25                  30
229  Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
230           35                  40                  45
231  Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
232       50                  55                  60
233  Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
234  65                  70                  75                  80
235  Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
236                   85                  90                  95
237  Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
238               100                 105                 110
239  Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
240           115                 120                 125
241  Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
242       130                 135                 140
243  Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
244  145                 150                 155                 160
245  Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Ala Gly
246               165                 170                 175
247  Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu Pro Leu Glu Arg
248               180                 185                 190
249  Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His Val Val Tyr Arg
250           195                 200                 205
251  Arg Glu Ala Val Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His
252       210                 215                 220
253  Asn Glu Ala Phe Gly Leu Gly Asp Leu Pro Asn Leu Leu Gly Leu Val
254  225                 230                 235                 240
255  Gly Asp Gln Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro
256           245                 250                 255
257  Gly Ser Tyr Ser Ile Glu Val Leu Leu Val Val Asp Asp Ser Val Val
258           260                 265                 270
259  Arg Phe His Gly Lys Glu His Val Gln Asn Tyr Val Leu Thr Leu Met
260           275                 280                 285
261  Asn Ile Val Asp Glu Ile Tyr His Asp Glu Ser Leu Gly Val His Ile
262           290                 295                 300
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/938,330

DATE: 09/10/2001
TIME: 09:23:47

Input Set : A:\LEX-0221-USA SEQLIST.txt
Output Set: N:\CRF3\09102001\I938330.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date